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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Mon Sep 24 11:16:20 EDT 2007

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Application No: 10580567 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-09-12 15:59:18.926
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 698 ms
Total Warnings: 8
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

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SEQUENCE LISTING

<110> NAKAMURA, Koji et al.

<120> METHOD OF DETECTING LIVER CANCER, DIAGNOSTIC FOR LIVER
CANCER AND REMEDY FOR CANCER

<130> 0760-0355PUS1

<140> 10580567

<141> 2007-09-12

<150> PCT/JP2004/017499

<151> 2004-11-25

<160> 10

<170> PatentIn version 3.1

<210> 1

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<220>

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<222> (174)..(1322)

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agccggaccc gcgcggcac cgctcccgaa accgcgaccc cggccggccca gag atg 176

Met

1

acc gcg acc gaa gcc ctc ctg cgc gtc ctc ttg ctc ctg ctg gct ttc 224

Thr Ala Thr Glu Ala Leu Leu Arg Val Leu Leu Leu Leu Ala Phe

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ggc cac agc acc tat ggg gct gaa tgc ttc ccg gcc tgc aac ccc caa 272

Gly His Ser Thr Tyr Gly Ala Glu Cys Phe Pro Ala Cys Asn Pro Gln

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aat gga ttc tgc gag gat gac aat gtt tgc agg tgc cag cct ggc tgg 320

Asn Gly Phe Cys Glu Asp Asp Asn Val Cys Arg Cys Gln Pro Gly Trp

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cag ggt ccc ctt tgt gac cag tgc gtg acc tct ccc ggc tgc ctt cac 368

Gln Gly Pro Leu Cys Asp Gln Cys Val Thr Ser Pro Gly Cys Leu His

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gga ctc tgt gga gaa ccc ggg cag tgc att tgc acc gac ggc tgg gac 416

Gly Leu Cys Gly Glu Pro Gly Gln Cys Ile Cys Thr Asp Gly Trp Asp

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ggg gag ctc tgt gat aga gat gtt cgg gcc tgc tcc tcg gcc ccc tgt	85	90	95	464
Gly Glu Leu Cys Asp Arg Asp Val Arg Ala Cys Ser Ser Ala Pro Cys				
gcc aac aac ggg acc tgc gtg agc ctg gac ggt ggc ctc tat gaa tgc	100	105	110	512
Ala Asn Asn Gly Thr Cys Val Ser Leu Asp Gly Gly Leu Tyr Glu Cys				
tcc tgt gcc ccc ggg tac tcg gga aag gac tgc cag aaa aag gac ggg	115	120	125	560
Ser Cys Ala Pro Gly Tyr Ser Gly Lys Asp Cys Gln Lys Lys Asp Gly				
ccc tgt gtg atc aac ggc tcc ccc tgc cag cac gga ggc acc tgc gtg	130	135	140	608
Pro Cys Val Ile Asn Gly Ser Pro Cys Gln His Gly Thr Cys Val				
gat gat gag ggc cgg gcc tcc cat gcc tcc tgc ctg tgc ccc cct ggc	150	155	160	656
Asp Asp Glu Gly Arg Ala Ser His Ala Ser Cys Leu Cys Pro Pro Gly				
ttc tca ggc aat ttc tgc gag atc gtg gcc aac agc tgc acc ccc aac	165	170	175	704
Phe Ser Gly Asn Phe Cys Glu Ile Val Ala Asn Ser Cys Thr Pro Asn				
cca tgc gag aac gac ggc gtc tgc act gac att ggg ggc gac ttc cgc	180	185	190	752
Pro Cys Glu Asn Asp Gly Val Cys Thr Asp Ile Gly Gly Asp Phe Arg				
tgc cgg tgc cca gcc ggc ttc atc gac aag acc tgc agc cgc ccc gtg	195	200	205	800
Cys Arg Cys Pro Ala Gly Phe Ile Asp Lys Thr Cys Ser Arg Pro Val				
acc aac tgc gcc agc agc ccc tgc cag aac ggg ggc acc tgc ctg cag	210	215	220	848
Thr Asn Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Thr Cys Leu Gln				
cac acc cag gtg agc tac gag tgt ctg tgc aag ccc gag ttc aca ggt	230	235	240	896
His Thr Gln Val Ser Tyr Glu Cys Leu Cys Lys Pro Glu Phe Thr Gly				
ctc acc tgt gtc aag aag cgc gcg ctg agc ccc cag cag gtc acc cgt	245	250	255	944
Leu Thr Cys Val Lys Lys Arg Ala Leu Ser Pro Gln Gln Val Thr Arg				
ctg ccc agc ggc tat ggg ctg gcc tac cgc ctg acc cct ggg gtg cac	260	265	270	992
Leu Pro Ser Gly Tyr Gly Leu Ala Tyr Arg Leu Thr Pro Gly Val His				
gag ctg ccc gtg cag cag ccc gag cac cgc atc ctg aag gtg tcc atg	275	280	285	1040
Glu Leu Pro Val Gln Gln Pro Glu His Arg Ile Leu Lys Val Ser Met				
aaa gag ctc aac aag aaa acc cct ctc acc gag ggc cag gcc atc	290	295	300	1088
Lys Glu Leu Asn Lys Lys Thr Pro Leu Leu Thr Glu Gly Gln Ala Ile				
			305	

tgc ttc acc atc ctg ggc gtg ctc acc agc ctg gtg ctg ggc act		1136
Cys Phe Thr Ile Leu Gly Val Leu Thr Ser Leu Val Val Leu Gly Thr		
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gtg ggt atc gtc ttc ctc aac aag tgc gag acc tgg gtg tcc aac ctg		1184
Val Gly Ile Val Phe Leu Asn Lys Cys Glu Thr Trp Val Ser Asn Leu		
325	330	335
cgc tac aac cac atg ctg cgg aag aag aac ctg ctg ctt cag tac aac		1232
Arg Tyr Asn His Met Leu Arg Lys Lys Asn Leu Leu Gln Tyr Asn		
340	345	350
agc ggg gag gac ctg gcc gtc aac atc atc ttc ccc gag aag atc gac		1280
Ser Gly Glu Asp Leu Ala Val Asn Ile Ile Phe Pro Glu Lys Ile Asp		
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Met Thr Thr Phe Ser Lys Glu Ala Gly Asp Glu Glu Ile		
370	375	380
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ctgtccta at ctttgtggtg ttgcgtatct cttgtgtcaa atctggtgaa cgctacgctt		1442
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Gln Asn Gly Phe Cys Glu Asp Asp Asn Val Cys Arg Cys Gln Pro Gly		
35	40	45
Trp Gln Gly Pro Leu Cys Asp Gln Cys Val Thr Ser Pro Gly Cys Leu		
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His Gly Leu Cys Gly Glu Pro Gly Gln Cys Ile Cys Thr Asp Gly Trp		
65	70	75
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Asp Gly Glu Leu Cys Asp Arg Asp Val Arg Ala Cys Ser Ser Ala Pro		

85

90

95

Cys Ala Asn Asn Gly Thr Cys Val Ser Leu Asp Gly Gly Leu Tyr Glu
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Cys Ser Cys Ala Pro Gly Tyr Ser Gly Lys Asp Cys Gln Lys Lys Asp
115 120 125

Gly Pro Cys Val Ile Asn Gly Ser Pro Cys Gln His Gly Gly Thr Cys
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Val Asp Asp Glu Gly Arg Ala Ser His Ala Ser Cys Leu Cys Pro Pro
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Gly Phe Ser Gly Asn Phe Cys Glu Ile Val Ala Asn Ser Cys Thr Pro
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Asn Pro Cys Glu Asn Asp Gly Val Cys Thr Asp Ile Gly Gly Asp Phe
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Arg Cys Arg Cys Pro Ala Gly Phe Ile Asp Lys Thr Cys Ser Arg Pro
195 200 205

Val Thr Asn Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Thr Cys Leu
210 215 220

Gln His Thr Gln Val Ser Tyr Glu Cys Leu Cys Lys Pro Glu Phe Thr
225 230 235 240

Gly Leu Thr Cys Val Lys Lys Arg Ala Leu Ser Pro Gln Gln Val Thr
245 250 255

Arg Leu Pro Ser Gly Tyr Gly Leu Ala Tyr Arg Leu Thr Pro Gly Val
260 265 270

His Glu Leu Pro Val Gln Gln Pro Glu His Arg Ile Leu Lys Val Ser
275 280 285

Met Lys Glu Leu Asn Lys Lys Thr Pro Leu Leu Thr Glu Gly Gln Ala
290 295 300

Ile Cys Phe Thr Ile Leu Gly Val Leu Thr Ser Leu Val Val Leu Gly
305 310 315 320

Thr Val Gly Ile Val Phe Leu Asn Lys Cys Glu Thr Trp Val Ser Asn
325 330 335

Leu Arg Tyr Asn His Met Leu Arg Lys Lys Asn Leu Leu Leu Gln Tyr
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